Listing of the Claims:

This Listing replaces all the prior versions and listings of claims.

1. (Cancelled)

2. (Previously presented) A method of amplifying a hairpin structure comprising converting a double stranded nucleic acid into the hairpin structure, wherein the double stranded nucleic acid contains at least one sequence of interest, and is referred to as a template nucleic acid, and wherein the template nucleic acid has an upper strand with a 5' and a 3' end and a lower strand with a 5' and a 3' end, the method comprising ligating a first single stranded nucleic acid to the 5' end of the upper strand of the template nucleic acid, and ligating a second single stranded nucleic acid which is non-complementary to the first single stranded nucleic acid to the 3' end of the lower strand of the nucleic acid ligating a cap of single stranded nucleic acid to both the 5' end of the lower strand and the 3' end of the upper strand of the template nucleic acid, such that the 3'end of the upper strand and the 5' end of the lower strand are contiguous, creating the hairpin structure and further comprising performing polymerase chain reaction with a first primer that binds to at least a portion of the upper single stranded non-complementary region at the 5' end of the upper strand, and a second primer that binds to at least a portion of the lower single stranded non-complementary region at the 3' end of the lower strand.

3-5. (Cancelled)

6. (Currently amended) A method of amplifying a nucleic acid sequence of interest that generates a PCR-amplified product which is substantially free of polymerase-induced errors, comprising:

(a) converting the nucleic acid sequence of interest into a first hairpin DNA structure, wherein the sequence of interest comprises a double stranded nucleic acid, and is referred to as a template nucleic acid, and wherein the template nucleic acid has an upper strand with a 5' and a 3' end and a lower strand with a 5' and a 3' end, by ligating a first single stranded nucleic acid to the 5' end of the upper strand of the template nucleic acid, and ligating a second single stranded nucleic acid which is non-complementary to the first single stranded nucleic acid to the 3' end of the lower strand of the nucleic acid; and further comprising ligating a cap of a single stranded nucleic acid to both the 5' end of

the lower strand and the 3' end of the upper strand of the template nucleic acid, such that the 3'end of the upper strand and the 5' end of the lower strand are contiguous, creating the first hairpin structure;

(b) amplifying the first hairpin DNA structure using PCR with a first primer that binds to at least a portion of the first single stranded nucleic acid, and a second primer that binds to at least a portion of the second single stranded nucleic acid to produce a plurality of linear double stranded PCR products wherein the ~~region between the 5' and the 3' end~~ double stranded PCR product comprises [[the]] an amplified sequence of interest and its complementary sequence flanked 5' and 3' by the first and the second single-stranded nucleic acid sequences ~~that were present in the double stranded nucleic acid of step (a)~~;

(c) converting the linear double stranded PCR products into a plurality of second hairpin structures ~~comprising a double-stranded complementary region and a non-complementary single-stranded loop at the end of the double-stranded region by a method which induces denaturation of the linear double stranded PCR products followed by sudden renaturation wherein the plurality of the second hairpin structures are formed by hybridization of the amplified sequence of interest and its complementary sequence that are present in each denaturated single stranded PCR products flanked by the first and second single stranded non-complementary single stranded 5' and 3' nucleic acid sequences~~ by converting the linear double stranded PCR products into a plurality of second hairpin structures by a method which induced denaturation of the linear double stranded PCR products into single stranded PCR products followed by sudden renaturation, wherein the amplified sequence of interest and its complement within each single strand hybridize during renaturation, thereby forming a hairpin structure;

(d) identifying from the second hairpin structures mismatch containing hairpin structures that comprise gaps in binding between the sequence of interest and its complementary sequence in the double-stranded region of the second hairpin structure wherein the gaps are a result of polymerase-generated nucleotide changes, insertions, or deletions, and

(e) removing such mismatch containing hairpin structure, and collecting the DNA that contains no mismatches.

7. (Currently amended) The method of claim 6, wherein [[the]] a method which induces denaturation followed by sudden renaturation is selected from the group consisting of (a) heat denaturation followed by rapid cooling, (b) addition of sodium hydroxide followed by sudden neutralization of the solution, and (c) addition of formamide followed by sudden removal of formamide.

8. (Previously presented) The method of claim 6, wherein the mismatch containing hairpin structures that contain PCR-induced errors and that have a mismatch in the double stranded region are separated from hairpin DNAs which do not contain mismatches by a method which recognizes DNA containing a mismatch.

9. (Original) The method of claim 8, wherein the method which recognizes DNA containing mismatches is selected from the group consisting of dHPLC-mediated fraction collection, denaturing gradient gel electrophoresis (DGGE), constant denaturant gel electrophoresis (CDGE), constant denaturant capillary electrophoresis (CDCE), and an enzymatic-based separation method.

10. (Original) The method of claim 9, wherein the enzymatic-based separation method is performed either in solution or bound to a solid support, and the enzyme is at least one enzyme selected from the group consisting of mismatch-recognition enzymes MutS, MutY, and TDG; Cel I; resolvases; endonuclease V; cleavases, and exonucleases.

11. (Cancelled)

12. (Original) The method of claim 6, wherein one strand of the template nucleic acid is joined with a second, fully complementary nucleic acid strand such that the two strands are contiguous, and such that during amplification the polymerase copies both the upper strand of the template nucleic acid and the lower strand of the template nucleic acid in a single pass.

13. (Cancelled)

14. (Cancelled)

15. (Cancelled)

16. (Cancelled)

17. (Currently amended) The method of claim [[16]] 38, wherein the method of mutation or polymorphism detection is selected from the group consisting of PCR, PCR/RE/LCR, MutEx-ACB-PCR, RFLP analysis, and APRIL-ATM.

18-34. (Cancelled)

35. (Cancelled)

36. (Previously presented) The method of claim 6, wherein concentration of the first and the second primer in step (b) is equal to eachother ('regular' PCR).

37. (Previously presented) The method of claim 6, wherein concentration of the first and the second primer in step (b) is unbalanced ('asymmetric' PCR).

38. (New) The method of claim 8 further comprising an assay consisting of mutation detection, mutation analysis, polymorphism detection, polymorphism analysis, microsatellite analysis, cloning, and protein functional analysis of the separated hairpin DNAs which do not contain mismatches.